

WHAT IS CLAIMED IS:

1. An isolated or purified polypeptide comprising a sequence selected from the group consisting of SEQ ID NOS: 6, 10, 14, 26, 28, 30, 32, 34, 38, 42, 46, 58, 60, 62, 64, 66, 68, 72, 76, and 80.
- 5 2. An isolated or purified polypeptide comprising at least 10 consecutive amino acids of the polypeptides of Claim 1.
3. An isolated or purified polypeptide having at least 70% homology to the polypeptide of Claim 1 as determined by analysis with FASTA version 3.0t78 with the 25 default parameters.
- 10 4. An isolated or purified polypeptide having at least 99% homology to the polypeptide of Claim 1 as determined by analysis with FASTA version 3.0t78 with the default parameters.
5. An isolated or purified polypeptide having at least 70% homology to the polypeptide of Claim 2 as determined by analysis with FASTA version 3.0t78 with the default parameters.
6. An isolated or purified polypeptide having at least 99% homology to the polypeptide of Claim 2 as determined by analysis with FASTA version 3.0t78 with the default parameters.
7. An isolated or purified polypeptide comprising a sequence selected from the group consisting of SEQ ID NOS: 4, 8, 12, 16, 18, 20, 22, 24, 36, 40, 44, 48, 50, 52, 54, 56, 70, 74, and 78.
- 20 8. An isolated or purified polypeptide comprising at least 10 consecutive amino acids of the polypeptides of Claim 7.
9. An isolated or purified polypeptide having at least 70% homology to the polypeptides of Claim 7 as determined by analysis with FASTA version 3.0t78 with the default parameters.
- 25 10. An isolated or purified polypeptide having at least 99% homology to the polypeptides of Claim 7 as determined by analysis with FASTA version 3.0t78 with the default parameters.

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11. An isolated or purified polypeptide having at least 70% homology to the polypeptides of Claim 8 as determined by analysis with FASTA version 3.0t78 with the default parameters.
12. An isolated or purified polypeptide having at least 99% homology to the polypeptides of Claim 8 as determined by analysis with FASTA version 3.0t78 with 20 the default parameters.
13. A method of making a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 6, 10, 14, 26, 28, 30, 32, 34, 38, 42, 46, 58, 60, 62, 64, 66, 68, 72, 76, and 80 comprising introducing a nucleic acid encoding said polypeptide, said nucleic acid being operably linked to a promoter, into a host cell.
14. A method of making a polypeptide comprising at least 10 amino acids of a sequence selected from the group consisting of the sequences of SEQ ID NOS: 6, 10, 14, 26, 28, 30, 32, 34, 38, 42, 46, 58, 60, 62, 64, 66, 68, 72, 76, and 80 comprising introducing a nucleic acid encoding said polypeptide, said nucleic acid being operably linked to a promoter, into a host cell.
15. A method of making a polypeptide having a sequence selected from the group consisting of SEQ ID NOS: 4, 8, 12, 16, 18, 20, 22, 24, 36, 40, 44, 48, 50, 52, 54, 56, 70, 74, and 78 comprising introducing a nucleic acid encoding said polypeptide, said nucleic acid being operably linked to a promoter, into a host cell.
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16. A method of making a polypeptide comprising at least 10 amino acids of a sequence selected from the group consisting of the sequences of SEQ ID NOS: 4, 8, 12, 16, 18, 20, 22, 24, 36, 40, 44, 48, 50, 52, 54, 56, 70, 74, and 78 comprising introducing a nucleic acid encoding said polypeptide, said nucleic acid being operably linked to a promoter, into a host cell.
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